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FIG 12

Anti-KIR light variable regions

DF-200 light variable	(1)	M--ESQTLVFTSILLWLYGADGNIVMTQSPKSMSSMVGERTLTCKASEN	50
PAN2D-Light-variable	(1)	MDFQVQIFSFLISASVIMSRGQIVLTQSPASMSASVGERTLTCTASSS	
Consensus	(1)	Q F I I L A G N I V L T Q S P S M S S L G E R V L T L C A S	
DF-200 light variable	(49)	VVTNWSYQQKPEQSPKLLIYGASNRYLGVPDRFTGSGSAIDFTLTSS	100
PAN2D-Light-variable	(51)	VSSTLVWYQQKPGSSPKLWIYSTNLA\$GVPARF\$GSGS\$GTS\$GLTSS	
Consensus	(51)	V S Y L W Y Q Q K P S P K L I Y S N S G V P R F S G S G S A T F S L T I S S	
DF-200 light variable	(98)	QAEADIAVTCGQGYSPYTFGGGKLEIKR	131
PAN2D-Light-variable	(101)	VEADAAVYCHQYERSPPTFGGGKLEIKR	
Consensus	(101)	M A E D A Y H C Q H P T F G G G T K L E I K R	

Numbers above amino acid sequences indicate position respective to initiation of translation Met (+1) in the immature (non-secreted) immunoglobulin. Underlined are the CDR regions

CDR's from the anti-KIR light variable regions

CDR-L1 from clones PAN-2D and DF-200		CDR -L2 from clones PAN-2D and DF-200
Residue before: Normally Cys. Residues after: Trp. Typically Trp-Tyr-Leu. Length: 10-17 aa		Residues before: Generally Ile-Tyr
Start: approximately 24 aa from the beginning of secreted protein		Length: 7 aa
DF-200 light variable (44) KASENVT- <u>YVS</u> (SEQ ID NO:3)		Start: approximately 16 aa after the end of CDR-L1
PAN2D-Light-variable (46) TASSVS\$SYLY (SEQ ID NO:4)		DF-200 light variable (70) GASNRYT (SEQ ID NO:5)
Consensus AS V S YL (SEQ ID NO:14)		PAN2D-Light-variable (73) STSNLAS (SEQ ID NO:6)
Consensus AS V S YL (SEQ ID NO:14)		Consensus SN S (SEQ ID NO:15)
CDR-L3 from clones PAN-2D and DF-200		
Residues before: Cys		
Residues after: Phe-Gly-XXX-Gly		
Length: 7-11 aa		
Start: approximately 33 aa after the end of CDR-L2		
DF-200 light variable (109) GQGYSYPYT (SEQ ID NO:7)		
PAN2D-Light-variable (112) HQYERSPEPT (SEQ ID NO:8)		
Consensus Q H P T (SEQ ID NO:16)		

FIG 13

>DF-200\VH\immature-PROT
MAVLGLLFLCLVTFPSCVLS
QVQLEQSGPGLVQPSQSL SITCTVSGFSFTPYGVHVVRRQSPGKGLEWLGVWSSGGNTDYNAAFISRLSINKDNSKSQVFFK
MNSLQVNDTAIYYCARNPRPGNYPYGM DYWGQGTSTVTSS (SEQ ID NO: 9)

Anti-KIR heavy variable regions (immature Fabs)

Sequences including CDR regions in heavy variable regions

CDR-H1 from clone DF-200 Residues before: Cys-XXX-XXX-XXX Residues after: Trp. Generally Trp-Val or Trp-Ile Length: 10-14 aa Start: Approximately 22-26 aa from the beginning of the secreted protein GFSFTPYGVH (SEQ ID NO: 10)	CDR-H2 from clone DF-200 Residues before: Leu-Glu-Trp-Ile-Gly but other variations possible Residues after: Lys or Arg / Leu or Ile or Val or Phe or Thr or Ala / Thr or Ser or Ile or Ala Length: 16-20 aa Start: Approximately 15 aa after the end of CDR-H1 VIWSSGGNTDYNAAFIS (SEQ ID NO: 11)
CDR-H3 from clones 4G1, 5D5 and 6C12 Residues before: Cys-XXX-XXX (Typically Cys-Ala-Arg) Residues after: Trp-Gly-XXX-Gly Length: 3-25 aa Start: Approximately 33 after the end of CDR-H2 NPRPGNYPYGM DY (SEQ ID NO: 12)	

The secreted, mature VH starts at:
Position 20: residue Q

The VH region ends with residue S and thereafter the constant region (not shown) continues